

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101664,859A  
Source: IFW/6  
Date Processed by STIC: 5-26-06

***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 05/26/2006

PATENT APPLICATION: US/10/664,859A

TIME: 12:16:26

Input Set : A:\Q77377 seq.ST25.txt

Output Set: N:\CRF4\05262006\J664859A.raw

3 <110> APPLICANT: BASLER, Konrad  
 4 BRUNNER, Erich  
 5 FROESCH, Barbara  
 6 KRAMPS, Thomas  
 7 PETER, Oliver  
 9 <120> TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING  
 PATHWAY  
 10 AND THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON  
 12 <130> FILE REFERENCE: Q77377  
 14 <140> CURRENT APPLICATION NUMBER: 10/664,859A  
 15 <141> CURRENT FILING DATE: 2003-09-22  
 17 <150> PRIOR APPLICATION NUMBER: US 09/915,543  
 18 <151> PRIOR FILING DATE: 2001-07-27  
 20 <150> PRIOR APPLICATION NUMBER: 60/221,502  
 21 <151> PRIOR FILING DATE: 2000-07-28  
 23 <160> NUMBER OF SEQ ID NOS: 25  
 25 <170> SOFTWARE: PatentIn version 3.3  
 27 <210> SEQ ID NO: 1  
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 29 <212> TYPE: DNA  
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 35 <222> LOCATION: (468)..(632)  
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 39 <222> LOCATION: (691)..(981)  
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 47 <222> LOCATION: (2394)..(4397)  
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 55 <222> LOCATION: (4927)..(6456)  
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 62 ttagcttaat acgatgctcc gaagtgttat tgcatttgca catatacata aaattgtgac 180  
 64 atagaatagg agaattccac atacaaatac aaaaatacaa aatcctccag taaaatttaa 240

(pg. 6)

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68 gtgagtgcct gcgtgcagtt cctgggtctaa atatgcttaa ttgcgttcgc cgacttcaaa      360
70 agcaataaaa cgatggattt taattgctac ttgagcaatt agccacacaa gggatcttgg      420
72 gaaggtcgat ttgaaggaat tcgatttcta ggatgctctc gacaaca atg ccc cgc      476
73                                     Met Pro Arg
74                                     1
76 agt cca acc caa caa cag ccg caa cca aac tcc gat gcc tcc tca aca      524
77 Ser Pro Thr Gln Gln Gln Pro Gln Pro Asn Ser Asp Ala Ser Ser Thr
78      5                      10                      15
80 agt gca tct gga tca aat cct gga gca gcg atc gga aat ggg gac tcg      572
81 Ser Ala Ser Gly Ser Asn Pro Gly Ala Ala Ile Gly Asn Gly Asp Ser
82 20                      25                      30                      35
84 gcg gcg agc aga agt tct ccg aag acc ctt aat agc gaa ccc ttt tct      620
85 Ala Ala Ser Arg Ser Ser Pro Lys Thr Leu Asn Ser Glu Pro Phe Ser
86                      40                      45                      50
88 act ttg tcg ccg ggtaagactt gtattgattt ctctttgtcc ggaattataa      672
89 Thr Leu Ser Pro
90                      55
92 caactttctg tgtttcca gat caa ata aaa ttg acg cca gaa gaa ggc act      723
93                      Asp Gln Ile Lys Leu Thr Pro Glu Glu Gly Thr
94                      60                      65
96 gag aaa agc gga cta tca act agt gat aaa gct gcc act gga gga gcc      771
97 Glu Lys Ser Gly Leu Ser Thr Ser Asp Lys Ala Ala Thr Gly Gly Ala
98                      70                      75                      80
100 cca ggc agt gga aat aat ctg ccc gag gga caa act atg cta agg cag      819
101 Pro Gly Ser Gly Asn Asn Leu Pro Glu Gly Gln Thr Met Leu Arg Gln
102                      85                      90                      95
104 aac tct acg agc aca atc aac tcg tgc cta gtc gct tct cca caa aac      867
105 Asn Ser Thr Ser Thr Ile Asn Ser Cys Leu Val Ala Ser Pro Gln Asn
106      100                      105                      110
108 tcc agt gaa cac tcg aat agc agc aat gtg tct gct aca gtg ggc ctt      915
109 Ser Ser Glu His Ser Asn Ser Ser Asn Val Ser Ala Thr Val Gly Leu
110 115                      120                      125                      130
112 act cag atg gta gat tgt gac gag caa tcg aag aaa aac aaa tgt agt      963
113 Thr Gln Met Val Asp Cys Asp Glu Gln Ser Lys Lys Asn Lys Cys Ser
114                      135                      140                      145
116 gtg aag gac gag gaa gct ggtaagactg ccctacaaat ggtttaaaat      1011
117 Val Lys Asp Glu Glu Ala
118                      150
120 tttaaaatgt attggcggtc acctttgtta atcattttaat tgtttttttt ttgctatact      1071
122 tacaatttta gttttaaact tgtaaacttg actaaaactc gcgaagctcg gatcaaaaca      1131
124 gacattttct tggaaccgta attaagctca taaaaatatt aattcatctt gatggaatgc      1191
126 atatcataga tgtactcaaa catctcaaga aagacctcaa attggatcaa ctaattagtt      1251
128 tgagaaaaaa ttgctgtact tttaagaata tattaattta aaaatttgct gagtgaaatg      1311
130 atataatagt cacaataatt tttagttaaa ctgctaaagc attttgaata gccgtgctac      1371
132 gcagatgcta ctagacgcgg tgtaaaagct aatttttatt taaaagctgt cctaattatc      1431
134 cataaccatt aatgtcccat ttca gaa ata agt tct aat aaa gca aaa ggt      1482
135                      Glu Ile Ser Ser Asn Lys Ala Lys Gly
136                      155                      160

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138 caa gca gct ggt ggc ggc tgc gaa aca ggt tct aca tcc agt ttg act 1530
139 Gln Ala Ala Gly Gly Gly Cys Glu Thr Gly Ser Thr Ser Ser Leu Thr
140      165      170      175
142 gtc aag gaa gaa ccc acc gat gtc tta ggc agt tta gta aat atg aaa 1578
143 Val Lys Glu Glu Pro Thr Asp Val Leu Gly Ser Leu Val Asn Met Lys
144      180      185      190
146 aaa gaa gaa aga gaa aat cat tcg cca acg atg tcc cct gtt ggt ttt 1626
147 Lys Glu Glu Arg Glu Asn His Ser Pro Thr Met Ser Pro Val Gly Phe
148      195      200      205
150 ggt tca att ggt aat gca cag gac aac tcc gct aca ccg ggtaagtttt 1675
151 Gly Ser Ile Gly Asn Ala Gln Asp Asn Ser Ala Thr Pro
152 210      215      220
154 aagagatcca tataaagcaa ataacaagaa ttaatgtcag ttaccaattt tatttgatag 1735
156 tcaaagaact actatagcga tatctcctgc cttttaattt tattttaatt aggaaatacg 1795
158 aatattttcta atttgtaaaa taaaattgat taattaacta gaatttaaaa accttttgaa 1855
160 ttaggacata cccttccaaa aatcagtaat cattgggaac gagagtgtgg tcccgaagga 1915
162 gactactata aaaccttttg agctatctga tactgcacgc tactaaaaat gattagttta 1975
164 ggaaaatggg tgtaattttg taggaagttt tcattttaga agaaatgtga ttattttatt 2035
166 aaacccttc aagcggaact acatttggtc tacgatattt tggaaaaaca aatggttaag 2095
168 ttggaaagtg cctataaaac agaattccac gggttcaaact actaaccagg tttttgattt 2155
170 aatttttgatt aatgagaaa ttatcacact tcagttaaaa tgtttaattc gattaaggtc 2215
172 ggacaatcac agcagatttc catttttgcg tgtatatata gaagtcgcct tcacactctt 2275
174 ctggcgcgct tcaccactac gtggagttcc gccgcgagtg atttatatag atgatttacg 2335
176 agttatttaa ttttttatgg tgtattttaa taaatatctt atttattcat tttacata 2393
178 gtt aaa att gaa aga att tca aac gac agt acc acg gaa aaa aaa gga 2441
179 Val Lys Ile Glu Arg Ile Ser Asn Asp Ser Thr Thr Glu Lys Lys Gly
180      225      230      235
182 tcg tcc ttg aca atg aat aat gac gaa atg agc atg gaa ggc tgc aat 2489
183 Ser Ser Leu Thr Met Asn Asn Asp Glu Met Ser Met Glu Gly Cys Asn
184      240      245      250
186 cag ttg aat ccc gat ttt atc aat gaa tct tta aat aat cct gca att 2537
187 Gln Leu Asn Pro Asp Phe Ile Asn Glu Ser Leu Asn Asn Pro Ala Ile
188 255      260      265      270
190 tcg agc ata tta gta agc gga gta gga cca ata ccc gga atc gga gtt 2585
191 Ser Ser Ile Leu Val Ser Gly Val Gly Pro Ile Pro Gly Ile Gly Val
192      275      280      285
194 gga gcg ggg acg gga aat tta ttg act gcc aac gcc aat gga atc tcc 2633
195 Gly Ala Gly Thr Gly Asn Leu Leu Thr Ala Asn Ala Asn Gly Ile Ser
196      290      295      300
198 tcg ggt agc agt aat tgt ttg gat tac atg caa cag caa aat cac ata 2681
199 Ser Gly Ser Ser Asn Cys Leu Asp Tyr Met Gln Gln Gln Asn His Ile
200      305      310      315
202 ttc gtg ttt tca act cag ctg gcc aac aaa ggg gcc gaa tca gtt tta 2729
203 Phe Val Phe Ser Thr Gln Leu Ala Asn Lys Gly Ala Glu Ser Val Leu
204      320      325      330
206 agc ggt caa ttt caa act att att gcg tat cac tgc act cag cct gct 2777
207 Ser Gly Gln Phe Gln Thr Ile Ile Ala Tyr His Cys Thr Gln Pro Ala
208 335      340      345      350
210 aca aaa agc ttc ctg gaa gac ttt ttt atg aaa aac cct tta aag att 2825

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212					355					360					365		
214	aac	aag	tta	cag	cgg	cac	aat	tcc	gtc	ggg	atg	cca	tgg	ata	ggc	atg	2873
215	Asn	Lys	Leu	Gln	Arg	His	Asn	Ser	Val	Gly	Met	Pro	Trp	Ile	Gly	Met	
216				370					375					380			
218	ggg	cag	gtt	gga	cta	act	cct	cct	aat	cct	gta	gcc	aaa	ata	aca	caa	2921
219	Gly	Gln	Val	Gly	Leu	Thr	Pro	Pro	Asn	Pro	Val	Ala	Lys	Ile	Thr	Gln	
220			385					390				395					
222	cag	cag	cca	cat	aca	aag	acc	gta	ggc	cta	ttg	aaa	ccc	caa	ttc	aat	2969
223	Gln	Gln	Pro	His	Thr	Lys	Thr	Val	Gly	Leu	Leu	Lys	Pro	Gln	Phe	Asn	
224		400					405					410					
226	caa	cat	gaa	aac	agc	aaa	cgt	agt	act	gta	agc	gcg	cct	agc	aac	tct	3017
227	Gln	His	Glu	Asn	Ser	Lys	Arg	Ser	Thr	Val	Ser	Ala	Pro	Ser	Asn	Ser	
228	415					420				425					430		
230	ttt	gtc	gac	cag	tct	gat	cct	atg	ggc	aac	gaa	act	gaa	ttg	atg	tgc	3065
231	Phe	Val	Asp	Gln	Ser	Asp	Pro	Met	Gly	Asn	Glu	Thr	Glu	Leu	Met	Cys	
232				435					440					445			
234	tgg	gaa	ggc	gga	tcc	tca	aac	acc	agt	agg	tct	gga	caa	aac	tca	cga	3113
235	Trp	Glu	Gly	Gly	Ser	Ser	Asn	Thr	Ser	Arg	Ser	Gly	Gln	Asn	Ser	Arg	
236			450					455				460					
238	aat	cat	gta	gac	agt	atc	agt	aca	tcc	agc	gag	tca	cag	gca	ata	aag	3161
239	Asn	His	Val	Asp	Ser	Ile	Ser	Thr	Ser	Ser	Glu	Ser	Gln	Ala	Ile	Lys	
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243	Ile	Leu	Glu	Ala	Ala	Gly	Val	Asp	Leu	Gly	Gln	Val	Thr	Lys	Gly	Ser	
244		480				485					490						
246	gat	cct	ggc	ctg	aca	act	gaa	aac	aac	att	gta	tca	ctg	caa	gga	gtt	3257
247	Asp	Pro	Gly	Leu	Thr	Thr	Glu	Asn	Asn	Ile	Val	Ser	Leu	Gln	Gly	Val	
248	495					500				505					510		
250	aag	gtt	cca	gac	gaa	aac	ctt	aca	cca	caa	cag	cgg	caa	cat	cgg	gaa	3305
251	Lys	Val	Pro	Asp	Glu	Asn	Leu	Thr	Pro	Gln	Gln	Arg	Gln	His	Arg	Glu	
252				515					520					525			
254	gaa	cag	ttg	gca	aaa	ata	aaa	aaa	atg	aat	caa	ttt	ctt	ttt	cct	gaa	3353
255	Glu	Gln	Leu	Ala	Lys	Ile	Lys	Lys	Met	Asn	Gln	Phe	Leu	Phe	Pro	Glu	
256			530					535				540					
258	aat	gag	aat	tca	gta	gga	gct	aat	gta	agc	tca	cag	ata	aca	aaa	att	3401
259	Asn	Glu	Asn	Ser	Val	Gly	Ala	Asn	Val	Ser	Ser	Gln	Ile	Thr	Lys	Ile	
260			545					550				555					
262	cca	gga	gat	tta	atg	atg	ggg	atg	tcg	ggg	ggc	gga	ggc	gga	tct	att	3449
263	Pro	Gly	Asp	Leu	Met	Met	Gly	Met	Ser	Gly	Gly	Gly	Gly	Gly	Ser	Ile	
264		560					565				570						
266	ata	aat	ccg	acg	atg	cga	caa	ctg	cat	atg	cca	ggg	aac	gcc	aaa	tcg	3497
267	Ile	Asn	Pro	Thr	Met	Arg	Gln	Leu	His	Met	Pro	Gly	Asn	Ala	Lys	Ser	
268	575					580				585					590		
270	gag	ctc	tta	tcg	gcg	aca	agt	tca	gga	ctt	tcg	gaa	gat	gta	atg	cat	3545
271	Glu	Leu	Leu	Ser	Ala	Thr	Ser	Ser	Gly	Leu	Ser	Glu	Asp	Val	Met	His	
272			595					600				605					
274	cca	ggg	gat	gtt	ata	tca	gat	atg	ggg	gcc	gta	ata	gga	tgt	aat	aat	3593
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279	Asn	Gln	Lys	Thr	Ser	Val	Gln	Cys	Gly	Ser	Gly	Val	Gly	Val	Val	Thr	
280			625					630				635					
282	gga	aca	act	gca	gct	gga	gta	aat	gtc	aat	atg	cat	tgc	tca	agc	tcc	3689
283	Gly	Thr	Thr	Ala	Ala	Gly	Val	Asn	Val	Asn	Met	His	Cys	Ser	Ser	Ser	
284		640					645					650					
286	ggc	gcc	ccg	aat	ggc	aat	atg	atg	gga	agc	tct	acg	gat	atg	cta	gcc	3737
287	Gly	Ala	Pro	Asn	Gly	Asn	Met	Met	Gly	Ser	Ser	Thr	Asp	Met	Leu	Ala	
288	655					660					665				670		
290	tcg	ttt	ggc	aac	aca	agc	tgc	aac	gtc	atc	gga	acg	gcc	cca	gat	atg	3785
291	Ser	Phe	Gly	Asn	Thr	Ser	Cys	Asn	Val	Ile	Gly	Thr	Ala	Pro	Asp	Met	
292					675				680						685		
294	tct	aag	gaa	gtt	tta	aat	caa	gat	agc	cga	acc	cat	tca	cat	caa	ggg	3833
295	Ser	Lys	Glu	Val	Leu	Asn	Gln	Asp	Ser	Arg	Thr	His	Ser	His	Gln	Gly	
296				690				695				700					
298	gga	gtt	gct	caa	atg	gag	tgg	tcg	aag	att	caa	cat	caa	ttt	ttc	gaa	3881
299	Gly	Val	Ala	Gln	Met	Glu	Trp	Ser	Lys	Ile	Gln	His	Gln	Phe	Phe	Glu	
300			705				710				715						
302	gaa	cgc	ctc	aag	ggg	ggc	aag	ccc	aga	caa	gtc	act	gga	act	gta	gta	3929
303	Glu	Arg	Leu	Lys	Gly	Gly	Lys	Pro	Arg	Gln	Val	Thr	Gly	Thr	Val	Val	
304		720					725				730						
306	cca	caa	cag	caa	acc	cct	tct	gga	tct	ggt	gga	aac	tcg	tta	aac	aac	3977
307	Pro	Gln	Gln	Gln	Thr	Pro	Ser	Gly	Ser	Gly	Gly	Asn	Ser	Leu	Asn	Asn	
308	735					740					745				750		
310	cag	gtg	cga	ccc	ctg	caa	ggt	cca	cct	cct	cct	tac	cac	tcc	atc	cag	4025
311	Gln	Val	Arg	Pro	Leu	Gln	Gly	Pro	Pro	Pro	Pro	Tyr	His	Ser	Ile	Gln	
312					755				760						765		
314	aga	tct	gcg	tca	gta	cca	ata	gcc	act	caa	tcg	ccc	aat	ccc	tcg	agt	4073
315	Arg	Ser	Ala	Ser	Val	Pro	Ile	Ala	Thr	Gln	Ser	Pro	Asn	Pro	Ser	Ser	
316				770				775				780					
318	cca	aac	aat	cta	tct	ctc	ccg	tca	ccg	cgg	aca	acc	gca	gca	gtc	atg	4121
319	Pro	Asn	Asn	Leu	Ser	Leu	Pro	Ser	Pro	Arg	Thr	Thr	Ala	Ala	Val	Met	
320			785					790				795					
322	gga	ttg	ccg	acc	aac	tct	cct	agc	atg	gat	gga	aca	gga	tca	tta	tct	4169
323	Gly	Leu	Pro	Thr	Asn	Ser	Pro	Ser	Met	Asp	Gly	Thr	Gly	Ser	Leu	Ser	
324		800					805				810						
326	gga	tct	gtt	ccg	caa	gct	aat	act	tcg	acg	gtt	cag	gca	ggc	aca	aca	4217
327	Gly	Ser	Val	Pro	Gln	Ala	Asn	Thr	Ser	Thr	Val	Gln	Ala	Gly	Thr	Thr	
328	815					820					825				830		
330	aca	gtg	ctc	tca	gca	aac	aag	aac	tgt	ttt	cag	gca	gac	acc	cca	tcg	4265
331	Thr	Val	Leu	Ser	Ala	Asn	Lys	Asn	Cys	Phe	Gln	Ala	Asp	Thr	Pro	Ser	
332				835				840				845					
334	ccg	tca	aat	caa	aat	cgt	agt	aga	aat	acc	gga	tcg	tca	agc	gtt	ctt	4313
335	Pro	Ser	Asn	Gln	Asn	Arg	Ser	Arg	Asn	Thr	Gly	Ser	Ser	Ser	Val	Leu	
336				850				855				860					
338	acg	cat	aac	tta	agc	agc	aac	cca	agt	acc	ccc	tta	tct	cat	cta	tcc	4361
339	Thr	His	Asn	Leu	Ser	Ser	Asn	Pro	Ser	Thr	Pro	Leu	Ser	His	Leu	Ser	
340			865					870				875					



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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:24; Xaa Pos. ~~1,2,7,8,12,15,18,21,22,25,26,27~~  
Seq#:25; Xaa Pos. 1,2,4,5,6,8,9,13,14,16,17,18,19,20,21,22,23,24,28,29,30  
Seq#:25; Xaa Pos. 31,32,33

VERIFICATION SUMMARY

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L:2203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0

M:341 Repeated in SeqNo=24

L:2249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0

M:341 Repeated in SeqNo=25